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                  OR "CHRISTIANSEN GUNNAR"/AU)
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                 OR ("KNUDSEN KATRINE"/AU OR "KNUDSEN KATRINE"/IN)
L5             8 SEA FILE=HCAPLUS ("MYGIND P H"/AU OR "MYGIND PER"/AU OR
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L6            54 SEA FILE=HCAPLUS L1 AND L2
L7             0 SEA FILE=HCAPLUS L3 AND L4 AND L5 AND L6
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M. Smith 308-3278

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L6 ANSWER 1 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:732281 HCAPLUS
TITLE: Serological investigation of Mycoplasma genitalium in infertile women
AUTHOR(S): Clausen, Helle Friis; Fedder, Jens; Drasbek, Mette; Nielsen, Pernille K.; Toft, Bente; Ingerslev, Hans Jakob; **Birkelund, Svend; Christiansen, Gunna**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, Department of Molecular and Structural Biology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Hum. Reprod. (2001), 16(9), 1866-1874
CODEN: HUREEE; ISSN: 0268-1161
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Background: The role of Mycoplasma genitalium in the pathogenesis of pelvic inflammatory disease has not been characterized. Methods: Sera from 308 infertile women were investigated for antibodies to M. genitalium by immunoblotting. Women with tubal factor infertility (TFI) made up 132 of the patients, 67 of the women had an infertile male partner and 109 were infertile for unknown reasons. Results: Of the TFI patients 29 (22.0%) were seropos. to the major adhesin, MgPa, of M. genitalium vs. 11 (6.3%) in the group of women with normal tubes. No cross-reactions between MgPa and P1 of the related Mycoplasma pneumoniae were found. Besides, MgPa pos. sera were confirmed by immunoblotting using a cloned fragment of the C-terminal part of MgPa specific to M. genitalium. Chlamydia trachomatis is known to be able to cause infertility as a result of salpingitis. Therefore, the sera were tested against C. trachomatis using a com. ELISA test. Seventy-five (56.8%) of the TFI patients were seropos. to C. trachomatis. Eight (27.6%) TFI patients seropos. to MgPa were neg. to C. trachomatis. Conclusions: This study indicates that M. genitalium may be an independent risk factor in the development of an inflammatory process leading to scarring of the uterine tubes in women and thereby causing infertility.

L6 ANSWER 2 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:720238 HCAPLUS
TITLE: Characterization of a hypervariable region in the genome of Chlamydophila pneumoniae
AUTHOR(S): Daugaard, L.; **Christiansen, G.; Birkelund, S.**
CORPORATE SOURCE: The Bartholin Building, Department of Medical Microbiology and Immunology, University of Aarhus, DK-8000 C, Aarhus, Den.
SOURCE: FEMS Microbiol. Lett. (2001), 203(2), 241-248
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chlamydophila pneumoniae displays surprisingly little genomic variation, as seen by comparisons of the published genomes from three different isolates and sequencing of four different genes from different isolates. We have in the present study, however, demonstrated genomic variation between 10 C. pneumoniae isolates in the 11690-bp region between the two outer membrane protein genes pmp1 and pmp2. This region of the C. pneumoniae CWL-029 isolate contains seven C. pneumoniae-specific open reading frames (hb1-7, encoding hydrophobic beta-sheet-contg. proteins). We identified addnl. 12 open reading frames in the C. pneumoniae CWL-029 genome encoding hypothetical proteins with similarity to the seven hypothetical Hb-proteins. Compared to other isolates, genomic variation is seen to cause frame-shifting of three of the 19 hb-open reading frames, which are proposed to be three full-length genes and eight frame-shifted pseudogenes. The hypothetical proteins encoded by these proposed genes contain an N-terminally located highly hydrophobic stretch of 50-60 residues. A similar motif is found in all identified Chlamydia inclusion membrane proteins and therefore the Hb-proteins are candidate inclusion proteins.

L6 ANSWER 3 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:720224 HCAPLUS
TITLE: Differential expression of Pmp10 in cell culture infected with Chlamydia pneumoniae CWL029
AUTHOR(S): Pedersen, A. S.; **Christiansen, G.**; **Birkelund, S.**
SOURCE: FEMS Microbiol. Lett. (2001), 203(2), 153-159
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The complete genome of Chlamydia pneumoniae contains a total of 21 genes encoding polymorphic membrane proteins (Pmp). From this large Pmp family three genes, pmp8, pmp10 and pmp11, were cloned and antibodies against recombinant full-length Pmp proteins were produced. Indirect immunofluorescence microscopy of HEp-2 cells infected with C. pneumoniae CWL029 was performed with the Pmp antibodies in combination with a Chlamydia-specific anti-lipopolysaccharide (LPS) antibody. This double staining technique clearly showed that expression of Pmp10 was differential. Addnl. double staining with monoclonal antibodies to the surface of C. pneumoniae elementary bodies and the anti-LPS antibody resulted in identification of seven monoclonal antibodies that reacted identically to the Pmp10 antibody indicating that Pmp10 is an immunodominant protein. Finally, the mol. mechanism responsible for differential expression is suggested to be variation in the guanine residues in the polyG tract of pmp10.

L6 ANSWER 4 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:467428 HCAPLUS
TITLE: Evaluation of real-time quantitative PCR for identification and quantification of Chlamydia pneumoniae by comparison with immunohistochemistry
AUTHOR(S): Mygind, T.; **Birkelund, S.**; Falk, E.; **Christiansen, G.**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology,

Aarhus, DK-8000, Den.
SOURCE: J. Microbiol. Methods (2001), 46(3), 241-251
CODEN: JMIMDQ; ISSN: 0167-7012
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chlamydia pneumoniae is a common cause of community-acquired pneumonia and it has been assocd. with atherosclerosis. C. pneumoniae has usually been diagnosed by serol. using a microimmunofluorescence test, but more recently polymerase chain reaction (PCR) has been viewed as an advantageous alternative. We developed a quant. real-time PCR for detection of C. pneumoniae. Primers were targeted for the pmp4 gene, and the PCR fragment was detected real-time with a fluorescence resonance energy transfer probe set using a LightCycler instrument. The PCR was used on DNA released from 50 .mu.m sections of paraffin-embedded formalin-fixed lung tissue from exptl. infected mice. Thereby, the no. of C. pneumoniae genomes was detd. To our knowledge this is the first time quantification of C. pneumoniae DNA has been attempted on paraffin-embedded formalin-fixed tissue. C. pneumoniae-specific immunohistochem. (IHC) was done on 5 .mu.m sections adjacent to the sections used in PCR, and the no. of inclusions were counted in each section. Good correlation was found when comparing results from PCR and IHC, which is in contrast to many previous studies.

REFERENCE COUNT: 29
REFERENCE(S):
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(3) Boman, J; J Clin Microbiol 1999, V37(12), P3791 HCAPLUS
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(9) Kalman, S; Nat Genet 1999, V21(4), P385 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 5 OF 54 HCAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 2001:456220 HCAPLUS
DOCUMENT NUMBER: 135:73609

TITLE: Time-dependent expression and processing of a hypothetical protein of possible importance for regulation of the Chlamydia pneumoniae developmental cycle

AUTHOR(S): Vandahl, Brian Berg; Gevaert, Kris; Demol, Hans; Hoorelbeke, Bart; Holm, Arne; Vandekerckhove, Joel; **Christiansen, Gunna; Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.

SOURCE: Electrophoresis (2001), 22(9), 1697-1704
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chlamydia pneumoniae is an obligate intracellular human pathogen infecting epithelial cells of the upper respiratory tract. It is a Gram-neg.

bacteria and has a unique biphasic developmental cycle. In this study, we use two-dimensional gel electrophoresis in combination with radioactive labeling to investigate time-dependent expression and processing of C. pneumoniae proteins. We report on (i) the identification of a hypothetical protein which is expressed late in the developmental cycle and subsequently processed; we speculate that this protein may be of importance for the developmental cycle of Chlamydia; (ii) the identification of the major outer membrane protein in three different variants, which may all be present in vivo.

REFERENCE COUNT: 16
REFERENCE(S): (1) Gevaert, K; Electrophoresis 1997, V18, P2950 HCAPLUS
(2) Gevaert, K; Electrophoresis 1998, V19, P909 HCAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 6 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2001:371214 HCAPLUS
DOCUMENT NUMBER: 135:119326
TITLE: Proteome analysis of the Chlamydia pneumoniae elementary body
AUTHOR(S): Vandahl, Brian Berg; **Birkelund, Svend**; Demol, Hans; Hoorelbeke, Bart; **Christiansen, Gunna**; Vandekerckhove, Joel; Gevaert, Kris
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Electrophoresis (2001), 22(6), 1204-1223
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Chlamydia pneumoniae is an obligate intracellular human pathogen that causes acute and chronic respiratory tract diseases and that has been implicated as a possible risk factor in the development of atherosclerotic heart disease. C. pneumoniae cultivated in Hep-2 cells were 35S-labeled and infectious elementary bodies (EB) were purified. The EB proteins were sepd. by two-dimensional gel electrophoresis. Excised protein spots were in-gel digested with trypsin and peptides were concd. on reverse-phase chromatog. beads for identification anal. by matrix-assisted laser desorption/ionization-mass spectrometry. In the pH range from 3-11, 263 C. pneumoniae protein spots encoded from 167 genes were identified. These genes constitute 15% of the genome. The identified proteins include 31 hypothetical proteins. It has recently been suggested that EB should be able to synthesize ATP. This view may be strengthened by the identification of several proteins involved in energy metab. Furthermore, proteins have been found which are involved in the type III secretion app. important for pathogenesis of intracellular bacteria. Proteome maps and a table of all identified proteins have been made available on the world wide web at www.gram.au.dk.

REFERENCE COUNT: 45
REFERENCE(S):
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(3) Benz, I; Infect Immun 1992, V60, P13 HCAPLUS
(4) Bini, L; Electrophoresis 1996, V17, P185 HCAPLUS
(5) Campbell, L; Infect Immun 1990, V58, P93 HCAPLUS
(6) Christiansen, G; J Bacteriol 1993, V175, P1785 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 7 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:589645 HCAPLUS
DOCUMENT NUMBER: 133:263634
TITLE: Characterization of the variability of a 75-kDa membrane protein in Mycoplasma hominis
AUTHOR(S): Mygind, T.; **Birkelund, S.**; **Christiansen, G.**
CORPORATE SOURCE: Dep. Med. Microbiol. Immunol., Bartholin Building, Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: FEMS Microbiol. Lett. (2000), 190(1), 167-176
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The gene p75 encoding a 75-kDa surface-exposed membrane protein P75 was cloned and sequenced from Mycoplasma hominis type strain PG21T. To investigate the intraspecies variability, sequences were obtained from an addnl. two isolates 7488 and 183, and the three sequences were compared. The nucleotide and amino acid differences were not confined to specific regions of the gene/protein, but when comparing the three sequences, differences were present as single site substitutions or small insertions or deletions of nucleotides/amino acids. The intraspecies variability was further investigated by restriction enzyme anal. with two restriction enzymes (AluI and MboII) of PCR products amplified from p75 from 28 M. hominis isolates. On the basis of band patterns produced by the two restriction enzymes, the isolates could be divided into five and six groups. These groups neither matched categories of the M. hominis vaa gene nor the M. hominis p120 gene classes, indicating that the three genes vary by different mechanisms and possibly indicating horizontal gene transfer.
REFERENCE COUNT: 28
REFERENCE(S):
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(5) Christiansen, G; Zbl Suppl 1990, V20, P535 HCAPLUS
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(7) Fraser, C; Science 1995, V270, P397 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 8 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:511104 HCAPLUS
DOCUMENT NUMBER: 134:99305
TITLE: Potential relevance of Chlamydia pneumoniae surface proteins to an effective vaccine
AUTHOR(S): **Christiansen, Gunna**; Pedersen, Anna-Sofie;

Hjerno, Karin; Vandahl, Brian; **Birkelund, Svend**
CORPORATE SOURCE: Departments of Medical Microbiology and Immunology, Aarhus, Den.
SOURCE: J. Infect. Dis. (2000), 181(Suppl. 3), S528-S537
CODEN: JIDIAQ; ISSN: 0022-1899
PUBLISHER: University of Chicago Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The surface of Chlamydia pneumoniae is covered with proteins but their exact identification is not known probably because of the presence of conformational epitopes. A family of 21 pmp genes has been found by DNA sequencing. In common, these genes have the capacity to encode the amino acid motif GGAI. Several of the genes have the capacity to encode outer membrane proteins of about 100 kDa. Thus, they are candidate genes to encode the protein(s) present in the 98-kDa protein band of the C. pneumoniae outer membrane complex. The prodn. of recombinant GGAI proteins is described as is the use of polyclonal antibodies raised against the recombinant GGAI proteins to det. their expression in C. pneumoniae elementary bodies. At least three of the proteins, Omp4, 5, and 11, are expressed.
REFERENCE COUNT: 30
REFERENCE(S):
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(2) Birkelund, S; Infect Immun 1989, V57, P2683 HCAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 9 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:454018 HCAPLUS
DOCUMENT NUMBER: 134:2362
TITLE: Genetic differences in the Chlamydia trachomatis tryptophan synthase .alpha.-subunit can explain variations in serovar pathogenesis
AUTHOR(S): Shaw, Allan C.; **Christiansen, Gunna**; Roepstorff, Peter; **Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: Microbes Infect. (2000), 2(6), 581-592
CODEN: MCINFS; ISSN: 1286-4579
PUBLISHER: Editions Scientifiques et Medicales Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The human pathogen Chlamydia trachomatis is an obligate intracellular bacterium, characterized by a developmental cycle that alternates between the infectious, extracellular elementary bodies and intracellular, metabolically active reticulate bodies. The cellular immune effector interferon gamma (IFN-.gamma.) inhibits chlamydial multiplication in human epithelial cells by induction of the tryptophan degrading enzyme indoleamine 2,3-dioxygenase. IFN-.gamma. causes persistent C. trachomatis

serovar A infections with atypical reticulate bodies that are unable to redifferentiate into elementary bodies and show diminished expression of important immunogens, but not of GroEL. However, the sensitivity to IFN-.gamma. varies among serovars of C. trachomatis. In our previous study significant IFN-.gamma.-specific, but tryptophan reversible, induction of proteins in C. trachomatis A and L2 with mol. masses of approx. 30 and 40 kDa was obsd. on 2D-gels. The 30-kDa protein from C. trachomatis L2 migrated with a significantly lower mol. wt. in C. trachomatis A. In this paper we include C. trachomatis B, C and D in our investigations and identify the proteins as alpha- and beta-subunits of the chlamydial tryptophan synthase using matrix-assisted laser desorption/ionization mass spectrometry. DNA sequencing of the trpA genes from C. trachomatis A and C shows that the TrpA in these serovars is a 7.7-kDa truncated version of C. trachomatis D and L2 TrpA. The truncation probably impairs the TrpA activity, thus elucidating a possible mol. mechanism behind variations in the pathogenesis of C. trachomatis serovars.

REFERENCE COUNT: 56
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 10 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:343954 HCAPLUS
DOCUMENT NUMBER: 133:348816
TITLE: Detection of Chlamydia trachomatis-specific antibodies in human sera by recombinant major outer-membrane protein polyantigens
AUTHOR(S): Mygind, Per; **Christiansen, Gunna**; Persson, Kenneth; **Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: J. Med. Microbiol. (2000), 49(5), 457-465
CODEN: JMMIAV; ISSN: 0022-2615
PUBLISHER: Lippincott Williams & Wilkins
DOCUMENT TYPE: Journal
LANGUAGE: English

AB This study was performed to generate and evaluate recombinant antigens for use in a species-specific C. trachomatis immunoassay. In a mol. genetic approach, fragments of the C. trachomatis major outer-membrane protein (MOMP) were produced as fusion proteins to create 3 different constructs encompassing the variable domains I, II and IV of selected C. trachomatis serovars. The recombinant MOMP polyantigens were affinity-purified and used in an ELISA. Antibody detection was evaluated with 103 patient sera and the results were compared with titers obtained in the micro-immunofluorescence test. The results showed that the generated MOMP polyantigens detected the presence of C. trachomatis-specific human antibodies with little cross-reaction to C. pneumoniae-specific

antibodies. When compared to the micro-immunofluorescence assay the MOMP polyantigen detected the presence of anti-C. trachomatis IgG antibodies with a sensitivity of 80% and a specificity of 91%.

REFERENCE COUNT: 35
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 11 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:285351 HCAPLUS
DOCUMENT NUMBER: 133:71196
TITLE: Membrane proteins PmpG and PmpH are major constituents of Chlamydia trachomatis L2 outer membrane complex
AUTHOR(S): Mygind, P. H.; **Christiansen, G.**; Roepstorff, P.; **Birkelund, S.**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: FEMS Microbiol. Lett. (2000), 186(2), 163-169
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The outer membrane complex of Chlamydia is involved in the initial adherence and ingestion of Chlamydia by the host cell. In order to identify novel proteins in the outer membrane of Chlamydia trachomatis L2, proteins were sepd. by sodium dodecyl sulfate polyacrylamide gel electrophoresis. By silver staining of the protein profile, a major protein doublet of 100-110 kDa was detected. In-gel tryptic digestion and matrix-assisted laser desorption/ionization mass spectrometry identified these proteins as the putative outer membrane proteins PmpG and PmpH.
REFERENCE COUNT: 22
REFERENCE(S):
(1) Altschul, S; Nucleic Acids Res 1997, V25, P3389 HCAPLUS
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 12 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 2000:60728 HCAPLUS
DOCUMENT NUMBER: 132:304112
TITLE: Cloning, sequencing and variability analysis of the gap gene from Mycoplasma hominis
AUTHOR(S): Mygind, T.; Zeuthen Sogaard, I.; Melkova, R.; Boesen, T.; **Birkelund, S.; Christiansen, G.**

CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: FEMS Microbiol. Lett. (2000), 183(1), 15-21
CODEN: FMLED7; ISSN: 0378-1097
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The gap gene encodes the glycolytic enzyme glyceraldehyde 3-phosphate dehydrogenase (GAPDH). The gene was cloned and sequenced from the Mycoplasma hominis type strain PG21T. The intraspecies variability was investigated by inspection of restriction fragment length polymorphism (RFLP) patterns after polymerase chain reaction (PCR) amplification of the gap gene from 15 strains and furthermore by sequencing of part of the gene in eight strains. The M. hominis gap gene was found to vary more than the Escherichia coli counterpart, but the variation at nucleotide level gave rise to only a few amino acid substitutions. To verify that the gene was expressed in M. hominis, a polyclonal antibody was produced and tested against whole cell protein from 15 strains. The enzyme was expressed in all strains investigated as a 36-kDa protein. All strains except type strain PG21T showed reaction to a 104-kDa band in addn. to the expected 36-kDa band. The protein reacting at 104 kDa is a M. hominis protein with either an epitope similar to one on GAPDH, or it is an Ig binding protein.

REFERENCE COUNT: 25
REFERENCE(S):
(1) Alexander, A; Infect Immun 1991, V59, P2147 HCAPLUS
(4) Christiansen, G; Int J Syst Bacteriol 1988, V38, P108 HCAPLUS
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(7) Guttman, D; Genetics 1994, V138, P993 HCAPLUS
ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 13 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:764647 HCAPLUS
DOCUMENT NUMBER: 132:206663
TITLE: Molecular biology of Chlamydia pneumoniae surface proteins and their role in immunopathogenicity
AUTHOR(S): **Christiansen, Gunna**; Boesen, Thomas; Hjerno, Karin; Daugaard, Lene; Mygind, Per; Madsen, Anna Sofie; Knudsen, Katrine; Falk, Erling; **Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology and the Department of Molecular and Structural Biology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: Am. Heart J. (1999), 138(5, Pt. 2), S491-S495
CODEN: AHJOA2; ISSN: 0002-8703
PUBLISHER: Mosby, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Background. The assocn. of Chlamydia pneumoniae with the development of atherosclerosis is based on serol. and on detection of C pneumoniae-specific DNA by polymerase chain reaction in the atheromas. Methods and Results. Because the humoral immune response frequently

recognizes epitopes present on the surface of the bacteria, we analyzed what components are present on the C. pneumoniae surface. We identified a family of proteins, the GGAl or Omp4-15 proteins, of which at least 3 are present on the surface of C. pneumoniae. We immunized rabbits with recombinant GGAl proteins and used these antibodies in immunofluorescence microscopy of exptl. infected mice. In lung sections, a massive infiltration with polymorph nuclear neutrophil cells was obsd. In the bronchial epithelial cells, C. pneumoniae inclusions were seen. Evidence was found of differential expression of the GGAl proteins. Conclusions. On the basis of surface localization, differential expression, and the fact that the proteins are recognized by the human humoral immune response, we speculate whether these proteins, in addn. to the lipopolysaccharides, are of importance for the immunopathogenesis of C pneumoniae.

REFERENCE COUNT: 13

REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 14 OF 54 HCAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:342767 HCAPLUS

DOCUMENT NUMBER: 131:42382

TITLE: Mapping and identification of interferon gamma-regulated HeLa cell proteins separated by immobilized pH gradient 2-dimensional gel electrophoresis

AUTHOR(S): Shaw, Allan Christian; Rossel Larsen, Martin; Roepstorff, Peter; Justesen, Just; **Christiansen, Gunna; Birkelund, Svend**

CORPORATE SOURCE: Department Medical Microbiology Immunology, University Aarhus, Aarhus, DK-8000, Den.

SOURCE: Electrophoresis (1999), 20(4-5), 984-993
CODEN: ELCTDN; ISSN: 0173-0835

PUBLISHER: Wiley-VCH Verlag GmbH

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Interferon .gamma. (IFN-.gamma.) is a potent immunomodulatory lymphokine, secreted by activated T-lymphocytes and NK-cells during the cellular immune response. Actions of IFN-.gamma. are mediated through binding to the IFN-.gamma.-receptor, present on most cells, and the subsequent activation of a great magnitude of IFN-.gamma. responsive genes was reported previously. IFN-.gamma.-regulated HeLa cell proteins were identified and mapped dy 2-D PAGE with the immobilized pH gradient (IPG) 2-D PAGE system. A semiconfluent layer of HeLa cells was grown on tissue culture plates, and changes in protein expression due to 100 U/mL IFN-.gamma. were investigated at different periods after treatment, using pulse labeling with [35S]Met/Cys in combination with 2-D PAGE (IPG). The identity of 8 protein spots was elucidated by matrix-assisted laser desorption/ionization-mass spectrometry (MALDI-MS), and several variants

of the IFN-.gamma.-inducible tryptophanyl-tRNA synthetase (hWRS) were detected by immunoblotting.

REFERENCE COUNT: 44

REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 15 OF 54 HCAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:342766 HCAPLUS

DOCUMENT NUMBER: 131:197411

TITLE: Mapping and identification of HeLa cell proteins separated by immobilized pH-gradient two-dimensional gel electrophoresis and construction of a two-dimensional polyacrylamide gel electrophoresis database

AUTHOR(S): Shaw, Allan Christian; Rossel Larsen, Martin; Roepstorff, Peter; Holm, Arne; **Christiansen, Gunna; Birkelund, Svend**

CORPORATE SOURCE: Department Medical Microbiology Immunology, University Aarhus, Aarhus, DK-8000, Den.

SOURCE: Electrophoresis (1999), 20(4-5), 977-983
CODEN: ELCTDN; ISSN: 0173-0835

PUBLISHER: Wiley-VCH Verlag GmbH

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The HeLa cell line, a human adenocarcinoma, is used in many research fields, since it can be infected with a wide range of viruses and intracellular bacteria. The mapping of HeLa cell proteins is useful for the investigation of parasite host cell interactions. Because of the recent improvements of 2-D gel electrophoresis with immobilized pH gradients (IPG) compared to isoelec. focusing with carrier ampholytes, a highly reproducible method for examg. global changes in HeLa cell protein expression due to different stimuli is now available. The authors have initiated the mapping of [35S]Met/Cys-labeled HeLa cell proteins with the 2-D PAGE (IPG)-system, using matrix-assisted laser desorption/ionization-mass spectrometry (MALDI-MS) and N-terminal sequencing for protein identification. To date 21 proteins were identified and mapped. To make these and future data accessible for interlab. comparison, the authors constructed a 2-D PAGE database on the World Wide Web.

REFERENCE COUNT: 18

REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 16 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:342738 HCAPLUS
DOCUMENT NUMBER: 131:72576
TITLE: Effects of interferon gamma on Chlamydia trachomatis serovar A and L2 protein expression investigated by two-dimensional gel electrophoresis
AUTHOR(S): Shaw, Allan Christian; **Christiansen, Gunna; Birkelund, Svend**
CORPORATE SOURCE: Department Medical Microbiology Immunology, University Aarhus, Aarhus, DK-8000, Den.
SOURCE: Electrophoresis (1999), 20(4-5), 775-780
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB C. trachomatis is an obligate intracellular bacterium causing human ocular and genital disease. The lymphokine interferon .gamma. (IFN-.gamma.) is an important immune effector exerting antimicrobial effects towards several intracellular parasites, the chlamydia included. IFN-.gamma. was reported to inhibit the chlamydial replication in vitro in part by depleting intracellular levels of tryptophan in a dose-dependent manner. Down-regulation of important immunogens was described. These findings are extended here, and the authors combined pulse labeling with [35S]Met and 2-D gel electrophoresis with immobilized pH gradients to investigate changes in the protein expression of C. trachomatis serovar A and L2 caused by treatment with IFN-.gamma.. In contrast to what was obsd. in C. trachomatis L2, the results showed that, in C. trachomatis A, down-regulations of the chlamydia major outer membrane protein and other proteins were detectable upon IFN-.gamma. treatment. The authors report the up-regulations of C. trachomatis A and L2 proteins with mol. masses of 30 kDa and 40 kDa which may be part of an, as yet, uncharacterized chlamydial response to IFN-.gamma. treatment.
REFERENCE COUNT: 25
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 17 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:27851 HCAPLUS
DOCUMENT NUMBER: 130:92748
TITLE: Outer membrane proteins of Chlamydia pneumoniae and the genes encoding them and their diagnostic and therapeutic uses
INVENTOR(S): **Birkelund, Svend**; Christiansen, Gunna; Knudsen, Katrine; Madsen, Anna-Sofie; Mygind, Per
PATENT ASSIGNEE(S): Den.
SOURCE: PCT Int. Appl., 115 pp.

CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9858953	A2	19981230	WO 1998-DK266	19980619
WO 9858953	A3	19990318		
W: AL, AM, AT, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, CZ, DE, DE, DK, DK, EE, EE, ES, FI, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG				
AU 9880119	A1	19990104	AU 1998-80119	19980619
EP 1007685	A2	20000614	EP 1998-928179	19980619
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
BR 9810288	A	20000919	BR 1998-10288	19980619

PRIORITY APPLN. INFO.: DK 1997-744 A 19970623
WO 1998-DK266 W 19980619

AB Members of a gene family from the human respiratory pathogen Chlamydia pneumoniae that encode surface exposed membrane proteins of a size of approx. 89-101 kDa and of 56-57 kDa, preferably about 89.6-100.3 kDa and about 56.1 kDa are cloned and characterized. The genes and gene products can be used in the diagnosis, pathol. and epidemiol. of C. pneumoniae and in vaccines. Genes were cloned by screening an expression library with antiserum to Chlamydia outer membrane complexes.

L6 ANSWER 18 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1999:25056 HCAPLUS
DOCUMENT NUMBER: 130:218977
TITLE: Identification of two novel genes encoding 97- to 99-kilodalton outer membrane proteins of Chlamydia pneumoniae
AUTHOR(S): Knudsen, Katrine; Madsen, Anna Sofie; Mygind, Per; **Christiansen, Gunna; Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: Infect. Immun. (1999), 67(1), 375-383
CODEN: INFIBR; ISSN: 0019-9567
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Two genes encoding 97- to 99-kDa Chlamydia pneumoniae VR1310 outer membrane proteins (Omp4 and Omp5) with mutual similarity were cloned and sequenced. The proteins were shown to be constituents of the C. pneumoniae outer membrane complex, and the deduced amino acid sequences were similar to those of putative outer membrane proteins encoded by the

Chlamydia psittaci and Chlamydia trachomatis gene families. By use of a monospecific polyclonal antibody against purified recombinant Omp4, it was shown that without heating, the protein migrated at 65 to 75 kDa in sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Immunoelectron microscopy showed that epitopes of Omp4 were exposed on the surface of C. pneumoniae elementary bodies, reticulate bodies, and outer membrane complex. Proteins encoded by the C. pneumoniae gene family seem to be dominant antigens in exptl. infected mice.

REFERENCE COUNT: 41
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 19 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:722395 HCAPLUS
DOCUMENT NUMBER: 130:63445
TITLE: Topological analysis of Chlamydia trachomatis L2 outer membrane protein 2
AUTHOR(S): Mygind, Per; **Christiansen, Gunna; Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: J. Bacteriol. (1998), 180(21), 5784-5787
CODEN: JOBAAY; ISSN: 0021-9193
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Using monospecific polyclonal antisera to different parts of Chlamydia trachomatis L2 outer membrane protein 2 (Omp2), we show that the protein is localized at the inner surface of the outer membrane. Omp2 becomes immunoaccessible when Chlamydia elementary bodies are treated with dithiothreitol, and protease digestions indicate that Omp2 has a possible two-domain structure.
REFERENCE COUNT: 28
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 20 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:620358 HCAPLUS
DOCUMENT NUMBER: 130:11161
TITLE: DNA sequencing reveals limited heterogeneity in the 16S rRNA gene from the rrnB operon among five Mycoplasma hominis isolates
AUTHOR(S): Mygind, Tina; **Birkelund, Svend;**

Christiansen, Gunna
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: Int. J. Syst. Bacteriol. (1998), 48(3), 1067-1071
CODEN: IJSBA8; ISSN: 0020-7713
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To investigate the intraspecies heterogeneity within the 16S rRNA gene of Mycoplasma hominis, five isolates with diverse antigenic profiles, variable/identical P120 hypervariable domains, and different 16S rRNA gene RFLP patterns were analyzed. The 16S rRNA gene from the rrnB operon was amplified by PCR and the PCR products were sequenced. Three isolates had identical 16S rRNA sequences and two isolates had sequences that differed from the others by only one nucleotide.
REFERENCE COUNT: 25
REFERENCE(S):
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ALL CITATIONS AVAILABLE IN THE RE FORMAT

L6 ANSWER 21 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:547882 HCAPLUS
DOCUMENT NUMBER: 129:287693
TITLE: Antigenic and genomic homogeneity of successive Mycoplasma hominis isolates
AUTHOR(S): Jensen, Lise T.; Thorsen, P.; Moller, B.; **Birkelund, S.; Christiansen, G.**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: J. Med. Microbiol. (1998), 47(8), 659-666
CODEN: JMMIAV; ISSN: 0022-2615
PUBLISHER: Lippincott-Raven Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Sixty M. hominis isolates were obtained from the cervices of pregnant women and from the ears or pharynges of their newborn babies. The isolates were examd. by SDS-PAGE and pulsed-field gel electrophoresis. Antigenic and genomic profiles were obtained for 16 series with 2 or more successive isolates. Both analyses led to the conclusion that isolates from the same woman were identical or nearly identical, while isolates from different women exhibited a high degree of variation with respect to both genomic and antigenic profiles.

L6 ANSWER 22 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:489146 HCAPLUS
DOCUMENT NUMBER: 129:212306
TITLE: The Mycoplasma hominis vaa gene displays a mosaic gene

structure
AUTHOR(S): Boesen, Thomas; Emmersen, Jeppe; Jensen, Lise T.; Ladefoged, Soren A.; Thorsen, Poul; **Birkelund, Svend; Christiansen, Gunna**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, The Bartholin Building, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Mol. Microbiol. (1998), 29(1), 97-110
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell Science Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Mycoplasma hominis contains a variable adherence-assocd. (vaa) gene. To classify variants of the vaa genes, we examd. 42 M. hominis isolates by PCR, DNA sequencing and immunoblotting. This uncovered the existence of five gene categories. Comparison of the gene types revealed a modular compn. of the Vaa proteins. The proteins constituted a conserved N-terminal part followed by a varying no. of interchangeable cassettes encoding approx. 110 amino acids with conserved sequence boxes flanking the cassettes. The interchangeable cassettes showed a high mutual homol. and a conserved leucine zipper motif. The smallest product contained only one cassette and the largest five. Addnl., two types of stop mutations caused by substitutions resulting in the expression of truncated Vaa proteins were obsd. Our results expand the known potential of the Vaa system in generating antigen variation.

L6 ANSWER 23 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:469401 HCAPLUS
DOCUMENT NUMBER: 129:243752
TITLE: Transmission electron microscopy and immunogold staining of mollicute surface antigens
AUTHOR(S): **Christiansen, Gunna; Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Den.
SOURCE: Methods Mol. Biol. (Totowa, N. J.) (1998), 104(Mycoplasma Protocols), 309-318
CODEN: MMBIED; ISSN: 1064-3745
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Mollicutes are cell wall-less bacteria. The mollicute cell membrane contains essentially all the cellular lipids and a substantial fraction of the cellular proteins; the molar ratio of lipid-to-protein is approx. 60:1. Both neg. staining and immunogold labeling of mollicutes are described here; Mycoplasma hominis is used as a specific example. Growth media for cultivation of the microorganisms; neg. staining with PTA (phosphotungstic acid) followed by electron microscopy; and immunogold staining using primary and secondary antibodies and colloidal gold, followed by electron microscopy, are described.

L6 ANSWER 24 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1998:328974 HCAPLUS
DOCUMENT NUMBER: 129:80346

TITLE: Analysis of the humoral immune response to Chlamydia outer membrane protein 2
AUTHOR(S): Mygind, Per; **Christiansen, Gunna**; Persson, Kenneth; **Birkelund, Svend**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus, DK-8000, Den.
SOURCE: Clin. Diagn. Lab. Immunol. (1998), 5(3), 313-318
CODEN: CDIMEN; ISSN: 1071-412X
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The humoral immune response to Chlamydia outer membrane protein 2 (Omp2) was studied. Omp2 is a highly genus-conserved structural protein of all Chlamydia species, contg. a variable N-terminal fragment. To analyze where the immunogenic parts were localized, seven highly purified truncated fusion proteins constituting different regions of the protein were produced (Chlamydia pneumoniae-Ompaa23-aa93, Chlamydia psittaci-Omp2aa23-aa94, and Chlamydia trachomatis-Omp2aa23-aa84, aa87-aa547, aa23-aa182, aa167-aa434, aa420-aa547). By an ELISA with serol. defined patient sera, Omp2 was a major immunogen of both C. pneumoniae and C. trachomatis infections (P .mchlt. 0.0001). The humoral immune responses were not confined to any particular region of the Omp2 protein, and no species-specific anti-Omp2 Igs were detected.

L6 ANSWER 25 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:583225 HCAPLUS
DOCUMENT NUMBER: 127:261105
TITLE: Chlamydia trachomatis utilizes the host cell microtubule network during early events of infection
AUTHOR(S): Clausen, Johannes D.; **Christiansen, Gunna**; Holst, Henrik U.; **Birkelund, Svend**
CORPORATE SOURCE: Departments of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Mol. Microbiol. (1997), 25(3), 441-449
CODEN: MOMIEE; ISSN: 0950-382X
PUBLISHER: Blackwell
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The host cell cytoskeleton is known to play a vital role in the life cycles of several pathogenic intracellular microorganisms by providing the basis for a successful invasion and by promoting movement of the pathogen once inside the host cell cytoplasm. McCoy cells infected with Chlamydia trachomatis serovars E or L2 revealed, by indirect immunofluorescence microscopy, co-location of microtubules and Chlamydia-contg. vesicles during the process of migration from the host cell surface to a perinuclear location. The vast majority of microtubule-assocd. Chlamydia vesicles also co-located with tyrosine-phosphorylated McCoy cell proteins. After migration, the Chlamydia-contg. vesicles were positioned exactly at the center of the microtubule network, indicating a microtubule-dependent mode of chlamydial redistribution. Inhibition of host cell dynein, a microtubule-dependent motor protein known to be involved in directed vesicle transport along microtubules, was obsd. to have a pronounced effect on C. trachomatis infectivity. Furthermore, dynein was found to co-locate with perinuclear aggregates of C. trachomatis E and L2 but not

C. pneumoniae VR-1310, indicating a marked difference in the cytoskeletal requirements for C. trachomatis and C. pneumoniae during early infection events. In support of this view, C. pneumoniae VR-1310 was shown to induce much less tyrosine phosphorylation of HeLa cell proteins during uptake than that seen for C. trachomatis.

L6 ANSWER 26 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:336552 HCAPLUS
DOCUMENT NUMBER: 127:62746
TITLE: Characterization of Chlamydia trachomatis L2-induced tyrosine-phosphorylated HeLa cell proteins by two-dimensional gel electrophoresis
AUTHOR(S): **Birkelund, Svend**; Bini, Luca; Pallini, Vitaliano; Sanchez-Campillo, Maria; Liberatori, Sabrina; Clausen, Johannes D.; Ostergaard, Soren; Holm, Arne; **Christiansen, Gunna**
CORPORATE SOURCE: Department Medical Microbiology Immunology, University Aarhus, Aarhus, DK-8000, Den.
SOURCE: Electrophoresis (1997), 18(3-4), 563-567
CODEN: ELCTDN; ISSN: 0173-0835
PUBLISHER: VCH
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Chlamydia trachomatis is an obligate intracellular bacterium, inducing its own uptake in nonprofessional phagocytes either by phagocytosis or pinocytosis. We have previously shown that C. trachomatis L2 induces tyrosine phosphorylation of eukaryotic proteins upon their entry by phagocytosis. In this paper we characterize the tyrosine-phosphorylated proteins by two-dimensional gel electrophoresis. In immunoblotting with anti-phosphotyrosine antibodies of C. trachomatis L2-infected HeLa cells, but not with uninfected cells, two rows of spots were obsd. with a mol. mass of 69 and 71 kDa and pI from 5.0 to 5.2. In addn., a single spot of 100 kDa and pI 6.2 was obsd.

L6 ANSWER 27 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1997:123519 HCAPLUS
DOCUMENT NUMBER: 126:250047
TITLE: The Mycoplasma hominis P120 membrane protein contains a 216 amino acid hypervariable domain that is recognized by the human humoral immune response
AUTHOR(S): Nyvold, Charlotte; **Birkelund, Svend**; **Christiansen, Gunna**
CORPORATE SOURCE: Department of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Microbiology (Reading, U. K.) (1997), 143(2), 675-688
CODEN: MROBEO; ISSN: 1350-0872
PUBLISHER: Society for General Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB In the antigenically heterogeneous species Mycoplasma hominis a monoclonal antibody, mAb 26.7D, was previously found to recognize a 120 kDa polypeptide from M. hominis 7488. This antibody did not react with the type strain PG21. The homologous gene from M. hominis PG21 was cloned and sequenced and found to have a sequence identity of 91% with the gene of

strain 7488. One hypervariable and two semivariable regions were detected. The epitope for mAb 26.7D was mapped to the hypervariable domain by expression of various parts of this domain in Escherichia coli using expression vector systems. A polyclonal antiserum (pAb 121) generated against the hypervariable region of P120 from PG21 identified the P120 homolog in M. hominis PG21. Fusion proteins of the hypervariable and const. parts of the proteins were constructed and tested for reactivity with 21 human sera. Twelve sera reacted with the 7488 hypervariable fusion protein, but only four reacted with the PG21 hypervariable fusion protein. No reactivity was seen with a fusion protein contg. part of the const. region of P120. Gene fragments amplified from 18 M. hominis isolates by PCR confirmed the heterogeneity of the hypervariable domain. Based on restriction endonuclease cleavage patterns of the hypervariable domain the 18 isolates could be divided into four classes. Reactivity with both mAb 26.7D and pAb 121 confirmed these classes. The hypervariable, but not the const., part of P120 was recognized by the human humoral immune response. Such a variable domain may be important in evasion of the host's immune response, and thus aid survival of the micro-organism.

L6 ANSWER 28 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:295775 HCAPLUS
DOCUMENT NUMBER: 125:2573
TITLE: Analysis of 0.5-kilobase-pair repeats in the Mycoplasma hominis lmp gene system and identification of gene products
AUTHOR(S): Ladefoged, Soeren A.; Jensen, Lise Torp; Brock, Birgitte; **Birkelund, Svend; Christiansen, Gunna**
CORPORATE SOURCE: Univ. Aarhus, Aarhus, Den.
SOURCE: J. Bacteriol. (1996), 178(10), 2775-2784
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Mycoplasma hominis, an opportunistic pathogenic bacterium of humans, has a small genome of 700 kb. Despite this, multiple copies of gene sequences with similarities to the structural gene (lmp1) of a 135-kDa surface-located membrane protein (Lmp1) have been identified on the genome of M. hominis PG21 (lmp2, lmp3, and lmp4). The distance between the lmp1-lmp2 region and the lmp3-lmp4 region was more than 110 kb. Lmp3-lmp4 of M. hominis PG21 was sequenced and found to contain two putative genes. The gene region of 6.5 kb contained a 5' unique region and a 3' unique region sepd. by 9 0.5-kb repeats with 51 to 90% similarity to 10 similar repeats found in the lmp1-lmp2 region. The 0.5-kb DNA repeats thus comprised about 1% of the entire genome. In both regions, a base change in one of the repeats gave rise to a stop codon, and thereby lmp2 and lmp4 occurred. By PCR amplification of reverse-transcriptase-generated cDNA it was shown that all four genes were transcribed. By use of Lmp-specific antibodies we showed that both lmp1 and lmp3 were translated into proteins (Lmp1 and Lmp3). Each of the four lmp genes represented by their unique cloned segments was used as a probe to analyze the presence, distribution, and organization of the genes within the genome in 13 M. hominis isolates. The repetitive element was detected at one or two locations on the chromosome for all isolates. The lmp3-specific element was present in all

isolates, and lmp1- and lmp2-specific elements were present in all but one isolate. The lmp4-specific element was present in about half the isolates tested. For five M. hominis isolates the chromosomal location of the lmp genes was mapped.

L6 ANSWER 29 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:286496 HCAPLUS
DOCUMENT NUMBER: 125:4975
TITLE: Purification of recombinant Chlamydia trachomatis histone H1-like protein Hc2, and comparative functional analysis of Hc2 and Hc1
AUTHOR(S): Pedersen, Lotte Bang; **Birkelund, Svend; Christiansen, Gunna**
CORPORATE SOURCE: Dep. of Medical Microbiology and Immunology, University of Aarhus, Aarhus C, DK-8000, Den.
SOURCE: Mol. Microbiol. (1996), 20(2), 295-311
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The metabolically inactive developmental form of Chlamydia trachomatis, the elementary body, contains two very basic DNA-binding proteins with homol. to eukaryotic histone H1. One of these, Hc1, is relatively well characterized and induces DNA condensation in vitro, whereas the other, Hc2, is functionally virtually uncharacterized. In this study we describe the purifn. of Hc2, and a detailed comparative functional anal. of Hc2 and Hc1 is presented. By gel shift assays and electron microscopy, marked differences in the nucleic acid-binding properties of Hc2 and Hc1 were obsd. Furthermore, Hc2 was found to strongly inhibit translation and transcription in vitro. Our results imply that DNA condensation is not the only function of Hc2.

L6 ANSWER 30 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:104880 HCAPLUS
DOCUMENT NUMBER: 124:225579
TITLE: Mapping of Chlamydia trachomatis proteins by Immobiline-polyacrylamide two-dimensional electrophoresis: spot identification by N-terminal sequencing and immunoblotting
AUTHOR(S): Bini, Luca; Sanchez-Campillo, Maria; Santucci, Annalisa; Magi, Barbara; Marzocchi, Barbara; Comanducci, Maurizio; **Christiansen, Gunna; Birkelund, Svend;** Cevenini, Roberto; et al.
CORPORATE SOURCE: Dep. Mol. Biol., Siena Univ., Siena, Italy
SOURCE: Electrophoresis (1996), 17(1), 185-90
CODEN: ELCTDN; ISSN: 0173-0835
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Proteins from purified elementary bodies of C. trachomatis were sepd. by 2-dimensional gel electrophoresis on nonlinear wide-range immobilized pH gradients in the first dimension and polyacrylamide gradient gels in the second dimension. The maps obtained with this system are highly reproducible and resolve .apprx.600 spots. By using immunoblot anal. with specific antibodies and/or N-terminal amino acid sequencing, the authors established the map positions of a no. of described chlamydial proteins,

such as the major outer membrane protein (MOMP) the 60 kDa cysteine-rich outer membrane protein (OMP2), the DnaK-like, GroEL-like, and macrophage infectivity potentiator (MIP)-like proteins, the plasmid-encoded pgp3 protein, two ribosomal proteins (S1 and L7/L12), and the protein-elongation factor EF-Tu. Other proteins, for which gene assignment was not possible, were identified by 3 parameters (Mr, pI and N-terminal sequence). This work provides a preliminary basis for a future and progressive compilation of a genome-linked database of chlamydial proteins.

L6 ANSWER 31 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1996:98222 HCAPLUS
DOCUMENT NUMBER: 124:139108
TITLE: The 18-kilodalton Chlamydia trachomatis histone H1-like protein (Hc1) contains a potential N-terminal dimerization site and a C-terminal nucleic acid-binding domain
AUTHOR(S): Pedersen, Lotte Bang; **Birkelund, Svend;** Holm, Arne; Ostergaard, Soren; **Christiansen, Gunna**
CORPORATE SOURCE: Department Medical Microbiology, University Aarhus, DK-8000, Den.
SOURCE: J. Bacteriol. (1996), 178(4), 994-1002
CODEN: JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The Chlamydia trachomatis histone H1-like protein (Hc1) is a DNA-binding protein specific for the metabolically inactive chlamydial developmental form, the elementary body. Hc1 induces DNA condensation in Escherichia coli and is a strong inhibitor of transcription and translation. These effects may, in part, be due to Hc1-mediated alterations of DNA topol. To locate putative functional domains within Hc1, polypeptides Hc12-57 and Hc153-125, corresponding to the N- and C-terminal parts of Hc1, resp., were generated. By chem. crosslinking with ethylene glycol-bis(succinic acid N-hydroxysuccinimide ester), purified recombinant Hc1 was found to form dimers. The dimerization site was located in the N-terminal part of Hc1 (Hc12-57). Moreover, CD measurements indicated an overall .alpha.-helical structure of this region. By using limited proteolysis, Southwestern blotting, and gel retardation assays, Hc153-225 was shown to contain a domain capable of binding both DNA and RNA. Under the same conditions, Hc12-57 had no nucleic acid-binding activity. Electron microscopy of Hc1-DNA and Hc153-125-DNA complexes revealed differences suggesting that the N-terminal part of Hc1 may affect the DNA-binding properties of Hc1.

L6 ANSWER 32 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:781405 HCAPLUS
DOCUMENT NUMBER: 123:193481
TITLE: Selection of Mycoplasma hominis PG21 deletion mutants by cultivation in the presence of monoclonal antibody 552
AUTHOR(S): Jensen, Lise Torp; Ladefoged, Soren; **Birkelund, Svend; Christiansen, Gunna**
CORPORATE SOURCE: Dep. Medical Microbiology and Immunology, Univ.

Aarhus, Aarhus, DK-8000, Den.
SOURCE: Infect. Immun. (1995), 63(9), 3336-47
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Three mutants of Mycoplasma hominis PG21 were isolated and shown to contain alterations in the size of a repeat-contg. gene encoding a surface-localized 135-kDa antigen designated Lmp1. The mutants were isolated by cultivating M. hominis for a 3-mo period in the presence of Lmp1-specific monoclonal antibody (MAb) 552. The epitope for MAb 552 was localized at the repeated part of the protein. The gene encoding Lmp1 is part of a transcriptional complex that contains 9.5 direct repeats of 471 bp each. Pure cultures of mutant strains were obtained by subcloning, and three mutants were characterized. The mutants showed deletions of a various no. of repeats. The deletions were accompanied by a decrease in size of the proteins. With increasing size of deletions, agglutination and growth inhibition by MAb 552 became less pronounced. Spontaneous aggregation of the mutant M. hominis cells in culture medium was, however, increased, indicating that the repeated elements may be of importance for repulsion of the cells.

L6 ANSWER 33 OF 54 HCAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1995:558162 HCAPLUS
DOCUMENT NUMBER: 123:103656

TITLE: Semi-nested polymerase chain reaction for detection of Pneumocystis carinii: implications for diagnosis, prevalence and predictive parameters

AUTHOR(S): Oestergaard, L.; Tarp, B.; Jensen, B. Nybo; Henriques, U.; **Birkelund, S.**; **Christiansen, G.**; Andersen, P. L.
CORPORATE SOURCE: Department of Infectious Diseases, Marselisborg Hospital, Aarhus, DK-8000, Den.

SOURCE: Immunol. Infect. Dis. (1995), 5(1), 59-66
CODEN: IINDEK; ISSN: 0959-4957
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The development of a semi-nested polymerase chain reaction (PCR) that provides semi-quantified results for detection of Pneumocystis carinii is described. The PCR was evaluated on bronchoalveolar lavage fluid and serum samples from HIV-infected patients with pulmonary impairment. When bronchoalveolar lavage fluid from 48 patients was examd., a prevalence of P. carinii pneumonia of 37.5% was found. The sensitivity and specificity of PCR were 94% and 97%, resp. Gomori methenamine silver staining showed a sensitivity and specificity of 59% and 100%, resp., and cytol. examn. consisting of Papanicolaou's and the May-Grunwald-Giemsa showed a sensitivity of 72% and a specificity of 100%. PCR did not detect P. carinii-DNA in serum obtained prior to clin. onset of P. carinii pneumonia. One of 7 serum samples obtained at the time of clin. P. carinii pneumonia was pos. by PCR. P. carinii pneumonia was the leading cause of pulmonary impairment both in patients receiving prophylactic antibiotic treatment against P. carinii and in patients not receiving prophylactic treatment. Toxoplasma gondii DNA was found by use of a nested PCR in bronchoalveolar lavage fluid from 3 patients. Cytomegalovirus (CMV) was isolated by quantitated culture in 66% of the

cases and the clin. course was not affected by positivity of CMV.

L6 ANSWER 34 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:279752 HCAPLUS
DOCUMENT NUMBER: 123:104016
TITLE: A 135-kilodalton surface antigen of Mycoplasma hominis PG21 contains multiple directly repeated sequences
AUTHOR(S): Ladefoged, Soren A.; **Birkelund, Svend**; Hauge, Steen; Brock, Birgitte; Jensen, Lise Torp; **Christiansen, Guanna**
CORPORATE SOURCE: Dep. Med. Microbiol. Immunol., Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: Infect. Immun. (1995), 63(1), 212-23
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A monoclonal antibody was used to characterize a 135-kDa surface-located membrane protein (Lmp1) generally present in Mycoplasma hominis strains. The monoclonal antibody, 552, was applied to identify the corresponding gene in an expression library of M. hominis PG21 DNA. The M. hominis PG21 lmp1 gene was sequenced, and its gene product was characterized with the goal of elucidating the structure and function of Lmp1. A total of 7196 bp in the lmp1 region was sequenced. An open reading frame of 4032 bp, encoding a protein of 1344 amino acids with a calcd. mol. wt. of 147,000, was identified. Anal. of the deduced amino acid sequence predicted a hydrophilic protein with a basic pI (10.0). The N-terminal 24 amino acids were a typical leader sequence. Downstream from the first 726 nucleotides, 6 similar direct repeats of 471 nucleotides were found. In repeat 7, a single-base substitution, C.fwdarw.A, gave rise to the stop codon of lmp1. Thus, the C-terminal 945 amino acids were encoded by the 471-bp direct repeats. As evidenced by Southern blot anal., the gene encoding the 135-kDa antigen is part of a multigene family. One of the genes, lmp2, was situated directly downstream from lmp1 where the direct repeats continued.

L6 ANSWER 35 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1995:33105 HCAPLUS
DOCUMENT NUMBER: 122:26123
TITLE: Analysis of a Mycoplasma hominis membrane protein, P120
AUTHOR(S): **Christiansen, Gunna**; Mathiesen, Soren L.; Nyvold, Charlotte; **Birkelund, Svend**
CORPORATE SOURCE: Institute of Medical Microbiology, The Bartholin Building, University of Aarhus, Aarhus-C, DK-8000, Den.
SOURCE: FEMS Microbiol. Lett. (1994), 121(1), 121-8
CODEN: FMLED7; ISSN: 0378-1097
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The monoclonal antibody MAb 26.7D generated against a clin. isolate of Mycoplasma hominis 7486 was shown to react with a surface-exposed epitope on a 120-kDa protein (P120). The gene encoding the protein was cloned and sequenced, and the transcriptional start point was detd. by primer extension anal. The gene contained an open reading frame of 3237 bp

encoding a peptide of 1079 amino acids with a deduced mol. mass of 123 kDa. A putative amino-terminal signal peptide and cleavage site for signal peptidase II were found. This suggests that the protein was synthesized as a precursor with subsequent processing to a mature lipoprotein. Surface exposure was confirmed by immunoelectron microscopy. Antibody mAb 26.7D reacted with 11 of 19 M. hominis strains. The gene was, however, present in all strains.

L6 ANSWER 36 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 199[illegible]:18529 HCAPLUS
DOCUMENT NUMBER: 122:37685
TITLE: Development of a nested polymerase chain reaction using time-resolved fluorometry for automated detection of Chlamydia trachomatis
AUTHOR(S): Oes[illegible]rgaard, L.; Moeller, J. K.; **Birkelund, S.**; C[illegible]**ristiansen, G.**; Andersen, P. L.
CORPORATE SOURCE: Mar[illegible]elisborg Hosp., Aarhus Univ. Hosp., Aarhus, DK-[illegible]000, Den.
SOURCE: Imm[illegible]nol. Infect. Dis. (1994), 4(1), 36-40
CODEN: IINDEK; ISSN: 0959-4957
DOCUMENT TYPE: Jou[illegible]al
LANGUAGE: Eng[illegible]sh
AB The polymerase chain re[illegible]tion (PCR) has proven successful for detection of Chlamydia trachomatis. [illegible]e development of a nested PCR for automated detection of amplified C. trachomatis DNA by use of time resolved fluorometry is describe[illegible]. The system was capable of detecting an amt. of DNA corresponding to le[illegible]s than one C. trachomatis genome when either purified C. trachomatis [illegible]NA or elementary bodies were used as target DNA. A correlation between t[illegible] amt. of fluorescence measured and the no. of C. trachomatis genomes was [illegible]en. Of 109 patient samples evaluated, seven were pos. by both cultu[illegible] and PCR. A hundred samples were neg. by both methods. Two samples w[illegible] pos. by PCR and neg. by culture. These two samples were from patie[illegible] who either had, or might have had, chlamydial infection. A clear dis[illegible]nction between pos. and neg. samples was obsd.

L6 ANSWER 37 OF 54 HCAPLU[illegible] COPYRIGHT 2001 ACS
ACCESSION NUMBER: 199[illegible]:678371 HCAPLUS
DOCUMENT NUMBER: 12[illegible]'8371
TITLE: Ch[illegible]terization of a linear epitope on Chlamydia tr[illegible]matis serovar L2 DnaK-like protein
AUTHOR(S): Bir[illegible]und, **Svend**; Larsen, Bente; Holm, Arne; Lun[illegible]ose, Anker G.; **Christiansen, Gunna**
CORPORATE SOURCE: Ins[illegible]Med. Microbiol., Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: In[illegible]. Immun. (1994), 62(5), 2051-7
CO[illegible] INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Jo[illegible]l
LANGUAGE: En[illegible]h
AB A cytoplasmic 75-kDa i[illegible]ogen from Chlamydia trachomatis serovar L2 has previously been charac[illegible]ed as being similar to the Escherichia coli heat shock protein Dna[illegible]e have localized a linear epitope for one monoclonal antibody spe[illegible]ic for C. trachomatis DnaK. By use of a recombinant DNA techni[illegible], the epitope was limited to 14 amino acids. With synthetic peptide[illegible]he epitope was further limited to eight amino

acids. Six of these amino acids are conserved in bovine HSP70, which has a known three-dimensional structure. The amino acid sequence homologous to the epitope is located in a linear part of the HSP70 mol. known as connect II.

L6 ANSWER 38 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:677861 HCAPLUS
DOCUMENT NUMBER: 121:277861
TITLE: Chlamydia trachomatis serovar L2 induces protein tyrosine phosphorylation during uptake by HeLa cells
AUTHOR(S): Birkelund, **Svend**; Johnsen, Helle; **Christiansen, Gunna**
CORPORATE SOURCE: Inst. Med. Microbiol., Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: Infect. Immun. (1994), 62(11), 4900-8
CODEN: INFIBR; ISSN: 0019-9567
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Chlamydia trachomatis is an obligate intracellular microorganism with a unique biphasic life cycle. The extracellular form, the elementary body (EB), is infectious but metabolically inactive. Attachment of EBs to host cells is mediated by a heparan sulfate-like glycosaminoglycan. Following attachment, the EB is internalized within a membrane-bound vesicle, and during the first 8 h of infection the vesicles are transported to a perinuclear location where they aggregate and fuse. By use of a monoclonal antibody against phosphotyrosine, the authors showed that three classes of proteins are tyrosine phosphorylated: a triple band of 68, 66, and 64 kDa, a 97-kDa band, and a 140-kDa band. The phosphorylation could be detected by immunoblotting from 15 min after infection of HeLa cells. The authors followed the movement of the EBs and the tyrosine phosphorylation of proteins by double-labeling immunofluorescence microscopy with the same monoclonal anti-phosphotyrosine antibody and a polyclonal antibody against the C. trachomatis L2 outer membrane complex. During the first 8 h of infection, the phosphorylation colocalized with EBs. Sixteen hours after infection, EBs have reorganized to the replicating reticulate bodies, forming an inclusion. At this time, phosphorylation was seen as dotted spots in the periphery of the inclusion.

L6 ANSWER 39 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1994:41694 HCAPLUS
DOCUMENT NUMBER: 120:41694
TITLE: Characterization of a Mycoplasma hominis gene encoding lysyl-tRNA synthetase (LysRS)
AUTHOR(S): Oz[illegible]n, Derya; **Birkelund, Svend**; **Christiansen, Gunna**
CORPORATE SOURCE: Inst. Med. Microbiol., Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: FEMS Microbiol. Lett. (1994), 116(3), 277-82
CODEN: FEMLED7; ISSN: 0378-1097
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The gene encoding lysyl-tRNA synthetase (lysS) in Mycoplasma hominis was cloned and sequenced. The gene has an open reading frame of 1466 bp

encoding a polypeptide with a predicted mol. mass of 57 kDa. The amino acid sequence showed 44.5 and 43.7% identity to the Escherichia coli lysyl-tRNA synthetases, encoded by lysS and lysU. Only one lysyl-tRNA synthetase encoding gene was found in M. hominis. The G + C content of the gene was 28.6%, which is significantly lower than in other prokaryotes. The gene was located 4 kb upstream of the M. hominis PG21 rRNA B operon.

L6 ANSWER 40 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 199[illegible]7163 HCAPLUS
DOCUMENT NUMBER: 120:[illegible]163
TITLE: Interaction of the Chlamydia trachomatis histone H1-like protein (Hc1) with DNA and RNA causes repression of transcription and translation in vitro
AUTHOR(S): Pedersen, Lotte Bang; **Birkelund, Svend;** **Christiansen, Gunna**
CORPORATE SOURCE: Inst. Med. Microbiol., Univ. Aarhus, Aarhus, DK-8000, Den.
SOURCE: Mol. Microbiol. (1994), 11(6), 1085-98
CODEN: MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Jou[illegible]
LANGUAGE: Eng[illegible]
AB The 18 kDa histone H1-like protein from Chlamydia trachomatis (Hc1) is a DNA-binding protein that is thought to be involved in condensation of the chlamydial chromosome during late stages in the chlamydial life cycle. Expression of Hc1 in Escherichia coli results in an overall relaxation of DNA and severely affects DNA, RNA and protein synthesis. The authors have analyzed the interaction of Hc1 with single-stranded DNA and RNA by Southwestern and northwestern blotting. Furthermore, the authors show that purified, recombinant Hc1 dramatically affects transcription and translation in vitro at physiol. relevant concns. These results were found to coincide with the formation of condensed Hc1-DNA and Hc1-RNA complexes as revealed by agarose gel electrophoresis and electron microscopy. The implications of these results for possible functions of Hc1 in vivo are discussed.

L6 ANSWER 41 OF 54 HCAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER: 19[illegible]667 HCAPLUS
DOCUMENT NUMBER: 11[illegible]567
TITLE: Use of polymerase chain reaction for detection of Chlamydia trachomatis. [Erratum to document cited in CA[illegible]:55202z]
AUTHOR(S): O[illegible]ard, Lars; **Birkelund, Svend;** C[illegible]ansen, **Gunna**
CORPORATE SOURCE: In[illegible]ed. Microbiol., Univ. Aarhus, Aarhus, DK-8000, D[illegible]
SOURCE: J[illegible]. Microbiol. (1993), 31(11), 3081
CODEN: JCMIDW; ISSN: 0095-1137
DOCUMENT TYPE: J[illegible]
LANGUAGE: En[illegible]
AB The errors were not re[illegible]ed in the abstr. or the index entries.

L6 ANSWER 42 OF 54 HCAP[illegible]PYRIGHT 2001 ACS
ACCESSION NUMBER: 1[illegible]562 HCAPLUS

DOCUMENT NUMBER: 119:...762
TITLE: Chl...ydia trachomatis Mip-like protein
AUTHOR(S): Lu...se, Anker G.; Rouch, Duncan A.; **Birkelund,** Sv... **Christiansen, Gunaa;** Pearce, Jo...
CORPORATE SOURCE: In...fied. Microbiol., Univ. Aarhus, Aarhus, DK-8000, De...
SOURCE: Mol...Microbiol. (1992), 6(17), 2539-48 CO...MOMIEE; ISSN: 0950-382X
DOCUMENT TYPE: Jou...
LANGUAGE: En...

AB A 27 kDa Chlamydia tr...tis Mip-like protein with homol. to a 175-amino-acid C-term...fragment of the surface-exposed Legionella pneumophila mip-gene ...t has previously been described. In this paper the entire chlamydia l...ke sequence of C. trachomatis serovar L2 [lymphogranuloma vene...LGV) biovar] is presented. The sequence shows high similarity to the...onella Mip protein and its C-terminal region, like that of the legio...Mip, has high amino acid similarity to eukaryotic and prokar...FK506-binding proteins. The chlamydial mip-like gene was def...by polymerase chain reaction (PCR) in other C. trachomatis serovars ...sequencing of the mip-like genes of serovars B and E (trachoma biova...shown to be highly conserved within the two majors biovars of C. ...matis. Monoclonal and polyclonal antibodies raised against the re...ant Mip-like protein failed to demonstrate surface-exposed epito...infectious elementary bodies or reproductive reticulate body forms ...by immunofluorescence or immuno-gold electron microscopy. However, ...plement-dependent inhibition of up to 91% of infectivity for cell ...s was obsd. with antibodies to the N-terminal fragment of the Mip-l...tein suggesting that antibody-accessible epitopes are present ...ectious EBs.

L6 ANSWER 43 OF 54 HCAP... COPYRIGHT 2001 ACS
ACCESSION NUMBER: 1...93014 HCAPLUS
DOCUMENT NUMBER: 1...:93014
TITLE: I...tion between the Chlamydia trachomatis histone H...protein (Hc1) and DNA
AUTHOR(S): C...nsen, **Gunna;** Pedersen, Lotte Bang; K... Jane E.; Lundemose, Anker G.; **Birkelund,** S...
CORPORATE SOURCE: I...fied. Microbiol., Univ. Aarhus, Aarhus, DK-8000, I...
SOURCE: J...eriol. (1993), 175(6), 1785-95 C...JOBAAY; ISSN: 0021-9193
DOCUMENT TYPE: J...
LANGUAGE: E...

AB The gene encoding th...chomatis Hc1 from serovar L2 was cloned into Escherichia coli by u...xpression vector pET11d. In this vector, transcription of the ...s under the control of a bacteriophage T7 promoter, and T7 RNA ...rase is inducible in the host. Following induction, the E. col...s were lysed gently. Gel filtration of the lysate revealed comig...of DNA and Hc1 in the voided vol. Electron microscopy revealed t...to be complexed with protein in large aggregates, often in ...rm of spherical bodies. Purified recombinant Hc1 maintained its D...ng capacity and was able at high concns. to

form condensed aggrega· ·ith DNA (one mol. of Hcl per base pair) independently of the : :r size of the DNA but with a slight preference for supercoiled DNA. : alone is thus able to package DNA into condensed spherical bodies.

L6 ANSWER 44 OF 54 HCAPL· OPYRIGHT 2001 ACS
ACCESSION NUMBER: 19 5623 HCAPLUS
DOCUMENT NUMBER: 11 623
TITLE: Us monoclonal antibodies for detection of antigen v on in Mycoplasma hominis
AUTHOR(S): L ed, Soren; Hauge, Steen; Andersen, Hans; Bi nd, **Svend; Christiansen, Gunna**
CORPORATE SOURCE: In ed. Microbiol., Univ. Aarhus, Aarhus, Den.
SOURCE: Z bl. Bakteriol., Suppl. (1990), 20(Recent Adv. M smol.), 634-9
C BASE2
DOCUMENT TYPE: J
LANGUAGE: E
AB The M. hominis is a h enous group of mycoplasmas commonly found in the female genital t· It is potentially pathogenic and may be involved in acute pel· flammatory disease, acute pyelonephritis and postpartum fever. In to analyze antigen variation in M. hominis, twelve monoclonal an· s (MAb) against M. hominis PG21 were produced. The MAb were classifi their epitopes in M. hominis PG21 were detd. By immunofluorescence· iton-X-114 sepn. it was detd. whether the epitopes were cytopl· urface localized or integral membrane proteins. Three MAb l with cytoplasmic antigens and their epitopes were all conserved i· er M. hominis strains. Nine MAb reacted with surface exposed prot· d all of these except one were shown to be integral membrane pr· By immunoblotting it was shown that only 3 of the surface exposed · cted with all the 25 other M. hominis strains while the remaining · ted with between 6 and 24 other M. hominis strains.

L6 ANSWER 45 OF 54 HCA· PYRIGHT 2001 ACS
ACCESSION NUMBER: 560 HCAPLUS
DOCUMENT NUMBER: 560
TITLE: monoclonal antibodies for detection of gene and variation in Mycoplasma hominis
AUTHOR(S): nsen, **Gunna**; Ladefoged, Soeren; teen; **Birkelund, Svend**; Andersen,
CORPORATE SOURCE: ed. Microbiol., Univ. Aarhus, Aarhus, Den.
SOURCE: l. Bakteriol., Suppl. (1990), 20(Recent Adv. mol.), 535-45
BASE2
DOCUMENT TYPE:
LANGUAGE:
AB Three monoclonal anti (MAb) against surface exposed M. hominis PG21 antigens were classi· d their epitopes in M. hominis PG21 were characterized. By T· 114 sepn. it was detd. whether the epitopes were integral membra ns. These MAb were used in immunoblotting to show the presence of genic epitope in 25 other M. hominis strains. Two MAb reacted with strains while the 3rd reacted only with 12

strains and in some st... with polypeptides different in size from the PG21 antigen. The MA... used to screen for recombinant E. coli contg. Sau3A contg. cleaved ... NA fragments ligated to the expression vectors pEX1, 2 and 3. Using ... id DNA from the recombinant clones as probes, Southern blotting anal... restriction enzyme cleaved DNA from 26 M. hominis strains was us... characterization; a variation in the hybridization patterns ... scribed. This variation was compared to the variation in immunoblo... results.

L6 ANSWER 46 OF 54 HCAP... COPYRIGHT 2001 ACS
ACCESSION NUMBER: ...-38 HCAPLUS
DOCUMENT NUMBER: ... 8
TITLE: ... trachomatis contains a protein similar to ...onella pneumophila mip gene products
AUTHOR(S): ..., A. G.; **Birkelund, S.**; Fey, S. J.; ...en, P.; **Christiansen, G.**
CORPORATE SOURCE: ...d. Microbiol., Univ. Aarhus, Aarhus, DK-8000, ...
SOURCE: ...robiol. (1991), 5(1), 109-15 ...MIEE; ISSN: 0950-382X
DOCUMENT TYPE: ...
LANGUAGE: ...

AB A 27 kDa C. trachoma... ...rotein was characterized by the use of monoclonal antibodie... ...two-dimensional gel electrophoresis. The protein was shown to ... ...ed in the membrane of reticulate bodies as well as elementary bo... ...its synthesis could be detected from 10 h post-infection. Clo... ...sequence anal. of the distal part of the gene revealed an open rea... ...s of 175 amino acids. Comparison of the deduced amino acid s... ...ith the NBRF data base revealed significant homol. between the 2... ...amydial membrane protein and the product of the macrophage infec... ...tentiator (mip) gene of L. pneumophila.

L6 ANSWER 47 OF 54 HCA... ...YRIGHT 2001 ACS
ACCESSION NUMBER: ...1 HCAPLUS
DOCUMENT NUMBER: ...
TITLE: ...lodalton cytoplasmic Chlamydia trachomatis L2 ...le is a DnaK-like protein
AUTHOR(S): ..., **Svend**; Lundemose, Anker G.; ...sen, **Gunna**
CORPORATE SOURCE: ... Microbiol., Univ. Aarhus, Aarhus C, ...Den.
SOURCE: ...mun. (1990), 58(7), 2098-104 ...FIBR; ISSN: 0019-9567
DOCUMENT TYPE: ...
LANGUAGE: ...

AB The gene coding for ... ...lodalton cytoplasmic C. trachomatis L2 polypeptide has been ... ...Escherichia coli, and the nucleotide sequence has been de... ...loned DNA fragment contained the coding region as well as th... ...promoter. The deduced amino acid sequence of the 1980-base-pai... ...ding frame revealed 94% homol. with a 75-kilodalton protei... ...trachomatis serovar D and 5% homol. with the DnaK proteins of E. ... ...of Bacillus megaterium, while amino acid homol. with human he... ...protein 70 (hsp70) was 42%. The promoter region was identifie... ...ter search and by primer extension of mRNA

synthesized in recombi... coli. The promoter region which differed from the putative pro... egion in serovar D was shown to be a mixed promoter type in whic...) region showed a regular TATA box configuration while th... egion showed high homol. with heat shock promoters. This mixed... er was recognized in E. coli.

L6 ANSWER 48 OF 54 HCAPL... YRIGHT 2001 ACS
ACCESSION NUMBER: 19... 8 HCAPLUS
DOCUMENT NUMBER: 11... 3
TITLE: C... ization and identification of early proteins i... ia trachomatis serovar L2 by two-dimensional g... ophoresis
AUTHOR(S): I... Anker G.; **Birkelund, Svend;** I... ter Mose; Fey, Stephen J.; C... en, **Gunna**
CORPORATE SOURCE: I... Microbiol., Univ. Aarhus, Aarhus, DK-8000, L...
SOURCE: I... mun. (1990), 58(8), 2478-86 C... IBR; ISSN: 0019-9567
DOCUMENT TYPE: J...
LANGUAGE: E...
AB The synthesis of ear... s from C. trachomatis serovar L2 was analyzed by two-dime... l electrophoresis. By pulse-label expts., the synthesis of sev... s was obsd. at 2 to 8 h postinfection before the major outer memb... in was detected at 8 to 10 h after infection. The early ... were synthesized throughout the 30-h period investigated, but th... s of three proteins of 75, 62, and 45 kilodaltons decreased ... to 30 h postinfection. Pulse-chase anal. showed that the signa... e same three proteins declined 26 to 30 h after infection. Th... early proteins were identified as the S1 ribosomal protein, t... ike protein, and DnaK-like protein, resp.

L6 ANSWER 49 OF 54 HCA... RIGHT 2001 ACS
ACCESSION NUMBER: ... 2 HCAPLUS
DOCUMENT NUMBER: 11...
TITLE: P... merase chain reaction for detection of C... rachomatis
AUTHOR(S): ... l, Lars; **Birkelund, Svend;** ... n, **Gunna**
CORPORATE SOURCE: ... Microbiol., Univ. Aarhus, Aarhus, DK-8000, ...
SOURCE: ... crobiol. (1990), 28(6), 1254-60 C... IDW; ISSN: 0095-1137
DOCUMENT TYPE: J...
LANGUAGE: E...
AB A polymerase chain re... R) assay was developed for detection of C. trachomatis DNA. Fr... ished sequence of the common C. trachomatis plasmid, two primer... elected. Detection of amplified sequences was done by agarose ... phoresis of cleaved or uncleaved amplified sequences, Southern ... on, or dot blot anal. The PCR assay was optimized and, after ... of amplification with primer set II, demonstrated a sensit... 0-17 g DNA, which corresponds to the detection of one copy ... lasmid. Because of the high sensitivity, a closed system was de... which airborne contamination was minimized.